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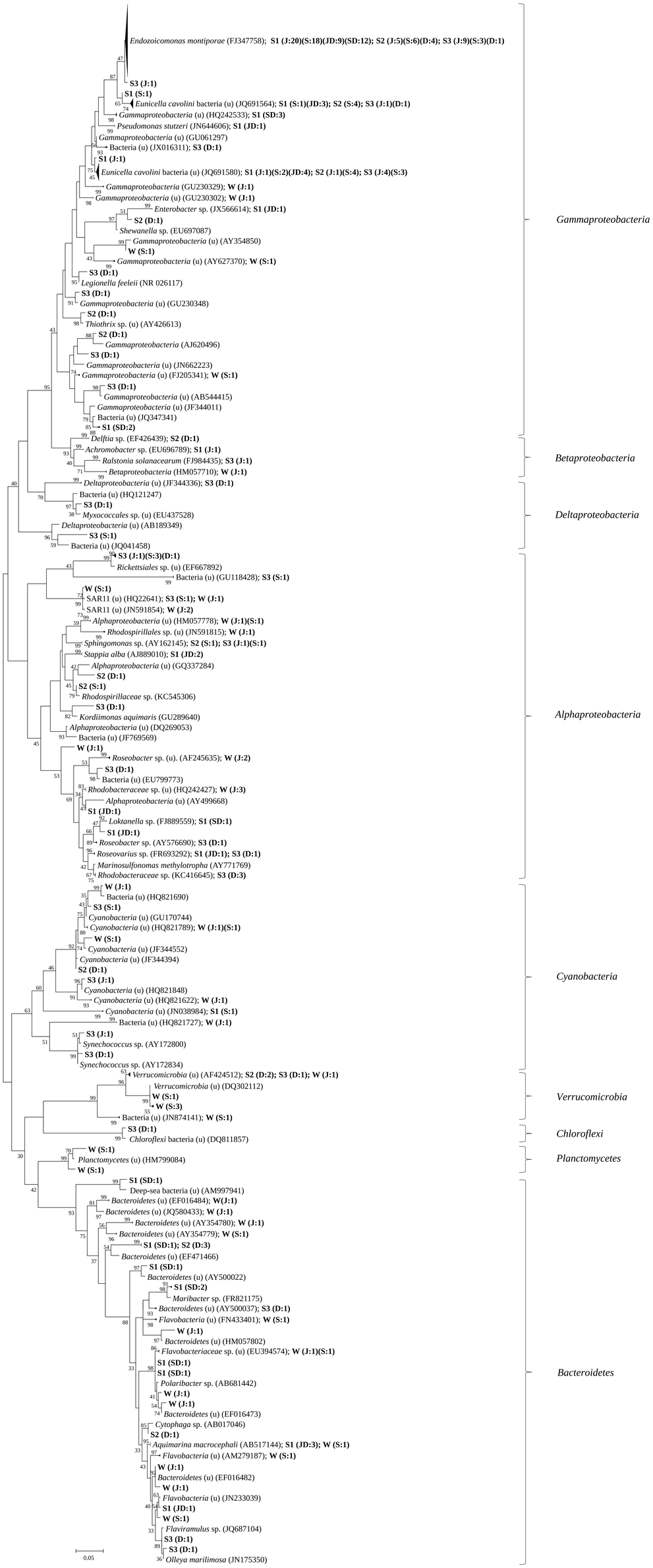

Figure 3b. Phylogenetic tree of reverse partial 16S rRNA gene sequences of clone libraries derived from sea water samples (W) and *Eunicella verrucosa* samples collected at sites 1 (S1), 2 (S2) and 3 (S3) in June (J), September (S), and when diseased (D). Numbers in brackets relate to number of clones from each library. Reference sequences include closest NCBI affiliations, which include bacteria previously isolated from corals and other marine invertebrates. The tree was calculated using the Maximum Likelihood method and Tamura-nei model as implemented in MEGA 5.1. Bootstrap values (500 replicates) are indicated on the branches. The scale bar corresponds to 0.05 substitutions per nucleotide position.